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Symbol	Name	Synonyms	Organism
PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	26S protease regulatory subunit 7, 26S proteasome AAA-ATPase subunit RPT1, MGC3004, MSS1, Nbla10058, Proteasome 26S subunit ATPase 2, Protein MSS1, S7	Homo sapiens

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UniProt

P35998,

Q9LIA5,

Q9UD13

IntAct

P35998

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OMIM

154365

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NCBI Gene

5701

NCBI RefSeq

NP_002794

NCBI RefSeq

NM_002803

NCBI UniGene

5701

NCBI Accession

BAE45763,

EAL24412

Homologues of PSMC2 ...

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Order by relevance

[HEC](#) is not a part of the 26 S proteasome and **interacts** with [MSS1](#) only when it is dissociated from the complex during [M phase](#). [1997]

[S2](#) [?] bound to two ATPases, [S4](#) and [S7](#) . [2000]

[S2](#) [?] formed an immunoprecipitable heterotrimer upon co-translation with [S4](#) and [S7](#) . [2000]

Concept 4
Implementation
by Robert Hoffmann

The non-ATPase S5b also formed a ternary complex with [S4](#) and [S7](#) and the three proteins assembled into a tetramer with [S2](#) [?]. [2000]

The use of chimeric ATPases demonstrated that [S2](#) [?] binds the NH(2)-terminal region of [S4](#) and the COOH-terminal two-thirds of [S7](#). [2000]

Mapping subunit contacts in the regulatory complex of the 26 S proteasome. [S2](#) [?] and S5b form a tetramer with ATPase subunits [S4](#) and [S7](#). [2000]

Our results suggest that [MSS1](#) has a key role in activation of [HIV](#) genes regulated by Tat. [1992]

Furthermore, we provide evidence that expression of [MSS1](#) enhances the Tat-mediated [transactivation](#). [1992]

The [MSS1](#) protein shares 42% sequence identity with the human TBP-1 protein, which binds Tat *in vitro* and suppresses Tat-mediated [transactivation](#) in vivo (ref. 6). We report here that the levels of [HIV](#) activation by Tat correlate with endogenous levels of [MSS1](#) messenger RNA. [1992]

Peptide sequencing identifies [MSS1](#), a modulator of [HIV](#) Tat-mediated [transactivation](#), as subunit 7 of the 26 S protease. [1993]

[Peptide sequence analysis](#) reveals that 22 amino acids from the N-terminus of subunit 7 correspond exactly to the N-terminus of [MSS1](#), a modulator of [HIV](#) gene expression. [1993]

These results show that [HEC](#) is a negative regulator of [MSS1](#) and suggest that it may modulate [M](#) phase progression, in part, through the regulation of proteasome-mediated degradation of [cell cycle](#) regulatory proteins. [1997]

Here the [nucleotide sequence](#) of a [Xenopus](#) homologue of the human [MSS1](#) gene, a positive modulator of the [HIV-1](#) Tat mediated [transactivation](#) in mammalian cells, is presented. [1995]

Additional internal peptides from subunit 7 obtained by CNBr cleavage also match 100% with the deduced [amino acid sequence](#) of [MSS1](#). [1993]

Based on the fact that directly sequenced peptides from subunit 7 are identical to more than 12% of the hypothetical translation product of [MSS1](#), and the fact that the [molecular weight](#) of subunit 7 (49 kDa) corresponds to the predicted [molecular weight](#) of [MSS1](#) (48,633 Da), we conclude that subunit 7 is [MSS1](#). [1993]

[Glycerol](#) [?] gradient sedimentation analysis revealed that [MSS1](#) is included in protein complexes whose density is lighter than that of the proteasome. [2000]

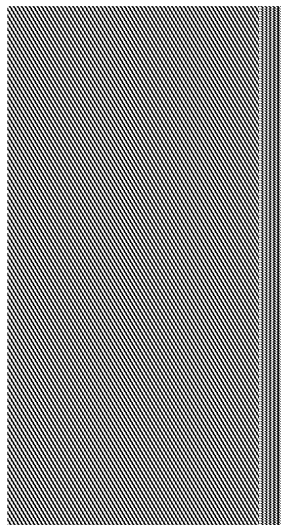
However, the ratio of [MSS1](#) to 20S varied greatly among tissues and [MSS1](#) was concentrated in the [thymus](#). [2000]

A homologue of the human [MSS1](#) gene, a positive modulator of [HIV-1](#) gene expression, is massively expressed in [Xenopus oocytes](#). [1995]

To recover the relationships among cichlasomatine genera and to test their monophyly we analyzed sequences from two mitochondrial (16S rRNA, [cytochrome b](#)) and one nuclear marker (first [intron](#) of [S7](#) [?] ribosomal gene) totalling 2236bp. [2008]

We present [DNA sequence](#) data from the mitochondrial [cytochrome b](#) ([cytb](#)) gene, the nuclear encoded [S7](#) [?] [intron 1](#), and discretely coded external morphological characters for all 20 species in the darter clade Nothonotus. [2008]





The phylogenies resulting from analysis of the morphological dataset lack resolution, but nodes present are found in the cytb and S7 [7] gene trees. [2008]



MSSP gene-2 encodes at least three alternative splicing products, MSSP-1 [?], MSSP-2, and Scr2, which have been implied to function as factors regulating DNA replication, transcription, apoptosis induction, and cell-cycle movement, via the interaction with C-MYC. [1998]



Please cite the use of iHOP as "Hofmann, R., Valencia, A. A gene network for navigating the literature. *Nature Genetics* 36, 664 (2004)" and as "iHOP - <http://www.ihop-net.org/>".

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